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Xendou\_ST25  
SEQUENCE LISTING

<110> Università degli Studi di Roma "La Sapienza"  
Consiglio Nazionale delle Ricerche

<120> Purification, cloning and biochemical characterization of xendou,  
endoribonucleasic activity involved in small nuclear RNA splicing independent  
biosynthesis in Xenopus laevis

<130> PCT25390

<150> IT RM2002A000365

<151> 2002-07-08

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 1268

<212> DNA

<213> Xenopus laevis

<220>

<221> exon

<222> (39)..(915)

<223>

<220>

<221> misc\_feature

<222> (1)..(38)

<223> 5' untranslated DNA region

<220>

<221> terminator

<222> (916)..(918)

<223>

<220>

<221> misc\_feature

<222> (916)..(1268)

<223> 3' untranslated DNA region

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atggggAAC tgggagcaga gagtgacggg caggagcc atg gcg agt aac agg ggg 56  
Met Ala Ser Asn Arg Gly  
1 5

cag ctg aac cat gaa ctc tcc aag ctg ttt aat gag ctg tgg gac gca 104  
Gln Leu Asn His Glu Leu Ser Lys Leu Phe Asn Glu Leu Trp Asp Ala  
10 15 20

gat cag aac cgg atg aag tcc ggg aag gat tat cgg atc tcc ttg cag 152  
Asp Gln Asn Arg Met Lys Ser Gly Lys Asp Tyr Arg Ile Ser Leu Gln  
25 30 35

ggt aaa gca ggg tac gta ccc gcc ggt tcc aac cag gcc agg gac agc 200  
Gly Lys Ala Gly Tyr Val Pro Ala Gly Ser Asn Gln Ala Arg Asp Ser  
40 45 50

gcc tcg ttc ccg ctc ttc cag ttc gtc gat gag gag aag ctg aag agc 248  
Ala Ser Phe Pro Leu Phe Gln Phe Val Asp Glu Glu Lys Leu Lys Ser  
55 60 65 70

agg aag acg ttt gca acc ttc att tcc ctg ctg gac aat tat gag atg 296  
Arg Lys Thr Phe Ala Thr Phe Ile Ser Leu Leu Asp Asn Tyr Glu Met  
75 80 85

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gac acg ggg gtg gcc gag gtt gtg act ccg gag gaa atc gct gaa aac Asp Thr Gly Val Ala Glu Val Val Thr Pro Glu Glu Ile Ala Glu Asn 90 95 100	344
aac aac ttc ctg gac gcc att ctg gaa acc aaa gtg atg aag atg gca Asn Asn Phe Leu Asp Ala Ile Leu Glu Thr Lys Val Met Lys Met Ala 105 110 115	392
cat gac tac ctg gtg agg aag aac caa gcc aaa ccc acc cggt aat gac His Asp Tyr Leu Val Arg Lys Asn Gln Ala Lys Pro Thr Arg Asn Asp 120 125 130	440
ttc aag gtc caa ctg tac aac atc tgg ttc cag ctg tac tca cggt gcc Phe Lys Val Gln Leu Tyr Asn Ile Trp Phe Gln Leu Tyr Ser Arg Ala 135 140 145 150	488
cca ggg agc aga ccc gat tcg tgc ggc ttt gag cac gtg ttt gtg gga Pro Gly Ser Arg Pro Asp Ser Cys Gly Phe Glu His Val Phe Val Gly 155 160 165	536
gaa tcg aag cga ggg cag gag atg atg ggg ctt cac aac tgg gtc cag Glu Ser Lys Arg Gly Gln Glu Met Met Gly Leu His Asn Trp Val Gln 170 175 180	584
ttt tac ctt cag gag aag agg aag aac atc gac tat aaa gga tac gtg Phe Tyr Leu Gln Glu Lys Arg Lys Asn Ile Asp Tyr Lys Gly Tyr Val 185 190 195	632
gct cgg cag aac aag agt cgg cgg gat gaa gat gat cag gtg ttg aac Ala Arg Gln Asn Lys Ser Arg Pro Asp Glu Asp Asp Gln Val Leu Asn 200 205 210	680
ctg cag ttc aat tgg aag gag atg gtg aaa ccc gtc ggc agc agc ttc Leu Gln Phe Asn Trp Lys Glu Met Val Lys Pro Val Gly Ser Ser Phe 215 220 225 230	728
att ggc gtc agc ccc gaa ttc gaa ttc gcc ctt tac acc atc gtc ttc Ile Gly Val Ser Pro Glu Phe Glu Phe Ala Leu Tyr Thr Ile Val Phe 235 240 245	776
ctc gcg tct cag gag aag atg agc cga gaa gtc gtt cgg ctg gaa gaa Leu Ala Ser Gln Glu Lys Met Ser Arg Glu Val Val Arg Leu Glu Glu 250 255 260	824
tac gaa ctg cag atc gtc gtc aat cgc cac ggc cgt tat ata ggg acc Tyr Glu Leu Gln Ile Val Val Asn Arg His Gly Arg Tyr Ile Gly Thr 265 270 275	872
gcc tac ccc gtc ctc ctg agc acc aat aac ccg gat ctg tac t Ala Tyr Pro Val Leu Leu Ser Thr Asn Asn Pro Asp Leu Tyr 280 285 290	915
gaggggcg ggcttagagat cacagccgt tccccacgggt tgggtgcatt tactaacaaa actgcaccaa tgcaacaaca atgcaagcag ataatgggg caggtccata tccctctgct ttccctagcg tgtgtgggc acattaaccc tataactgtc actcactgca ccagaccat tatttaaccc cacaagggac atcaagccag tgccctgtta tgagagagcg cagccgggc ttctctactg tgaaacttct gtattgtata gagttactt ggtttcttcc tccagacaat ttcacttttt ttttgcttg cctttaacca taaaaagtcc atgacatttc tgt	975 1035 1095 1155 1215 1268

<210> 2  
<211> 292  
<212> PRT

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&lt;213&gt; Xenopus laevis

&lt;400&gt; 2

Met Ala Ser Asn Arg Gly Gln Leu Asn His Glu Leu Ser Lys Leu Phe  
1 5 10 15

Asn Glu Leu Trp Asp Ala Asp Gln Asn Arg Met Lys Ser Gly Lys Asp  
20 25 30

Tyr Arg Ile Ser Leu Gln Gly Lys Ala Gly Tyr Val Pro Ala Gly Ser  
35 40 45

Asn Gln Ala Arg Asp Ser Ala Ser Phe Pro Leu Phe Gln Phe Val Asp  
50 55 60

Glu Glu Lys Leu Lys Ser Arg Lys Thr Phe Ala Thr Phe Ile Ser Leu  
65 70 75 80

Leu Asp Asn Tyr Glu Met Asp Thr Gly Val Ala Glu Val Val Thr Pro  
85 90 95

Glu Glu Ile Ala Glu Asn Asn Phe Leu Asp Ala Ile Leu Glu Thr  
100 105 110

Lys Val Met Lys Met Ala His Asp Tyr Leu Val Arg Lys Asn Gln Ala  
115 120 125

Lys Pro Thr Arg Asn Asp Phe Lys Val Gln Leu Tyr Asn Ile Trp Phe  
130 135 140

Gln Leu Tyr Ser Arg Ala Pro Gly Ser Arg Pro Asp Ser Cys Gly Phe  
145 150 155 160

Glu His Val Phe Val Gly Glu Ser Lys Arg Gly Gln Glu Met Met Gly  
165 170 175

Leu His Asn Trp Val Gln Phe Tyr Leu Gln Glu Lys Arg Lys Asn Ile  
180 185 190

Asp Tyr Lys Gly Tyr Val Ala Arg Gln Asn Lys Ser Arg Pro Asp Glu  
195 200 205

Asp Asp Gln Val Leu Asn Leu Gln Phe Asn Trp Lys Glu Met Val Lys  
210 215 220

Pro Val Gly Ser Ser Phe Ile Gly Val Ser Pro Glu Phe Glu Phe Ala  
225 230 235 240

Leu Tyr Thr Ile Val Phe Leu Ala Ser Gln Glu Lys Met Ser Arg Glu  
245 250 255

Val Val Arg Leu Glu Glu Tyr Glu Leu Gln Ile Val Val Asn Arg His  
Pagina 3

Gly Arg Tyr Ile Gly Thr Ala Tyr Pro Val Leu Leu Ser Thr Asn Asn  
275 280 285

Pro Asp Leu Tyr  
290

<210> 3  
<211> 20  
<212> RNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligoribonucleotide

<220>  
<221> misc\_RNA  
<222> (1)..(20)  
<223> Synthetic oligoribonucleotide which includes U16 upstream cleavage site

<400> 3  
ggaaacguau ccuuuuggqaq

20

<210> 4  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide

<220>  
<221> misc\_RNA  
<222> (1)..(20)  
<223> Mutant of SEQ ID 3

<220>  
<221> variation  
<222> (15)..(15)  
<223> "U" replaced by "G"

<220>  
<221> variation  
<222> (18)..(18)  
<223> "G" replaced by "A"

<220>  
<221> variation  
<222> (19)..(19)  
<223> "A" replaced by "G"

<220>  
<221> variation  
<222> (20)..(20)  
<223> "G" is replaced by "T"

<400> 4

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20

ggaaacguau ccuugggagt

<210> 5  
<211> 20  
<212> RNA  
<213> Artificial Sequence  
  
<220>  
<223> synthetic oligoribonucleotide  
  
<220>  
<221> misc\_RNA  
<222> (1)..(20)  
<223> Mutant of SEQ ID 3

<220>  
<221> variation  
<222> (14)..(14)  
<223> "U" is replaced by "C"

<400> 5  
ggaaacguau ccucugggag

20

<210> 6  
<211> 20  
<212> RNA  
<213> Artificial Sequence  
  
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<223> synthetic oligoribonucleotide  
  
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<221> misc\_RNA  
<222> (1)..(20)  
<223> Mutant of SEQ ID 3

<220>  
<221> variation  
<222> (14)..(14)  
<223> "U" is replaced by "G"

<400> 6  
ggaaacguau ccugugggag

20

<210> 7  
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<212> DNA  
<213> Artificial Sequence  
  
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<223> MAHs: synthetic degenerate oligonucleotide  
  
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<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer element  
  
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<221> modified\_base  
<222> (18)..(18)  
<223> "n" : I

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<220>  
<221> modified\_base  
<222> (6)..(6)  
<223> "n" : I

<400> 7  
atggcncayg aytayytngt

20

<210> 8  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> IGTa: synthetic degenerate oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer element

<220>  
<221> modified\_base  
<222> (3)..(3)  
<223> "n" : I

<220>  
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<222> (9)..(9)  
<223> "n" : I

<220>  
<221> modified\_base  
<222> (12)..(12)  
<223> "n": I

<220>  
<221> modified\_base  
<222> (15)..(15)  
<223> "n" : I

<220>  
<221> modified\_base  
<222> (18)..(18)  
<223> "n" : I

<400> 8  
acnggrtang cngtnccnat

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<210> 9  
<211> 27  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<220>

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<221> misc\_feature  
<222> (1)..(27)  
<223> Primer

<400> 9  
aagcttcttc atggcggctc ggccaat

27